FIG. 1A

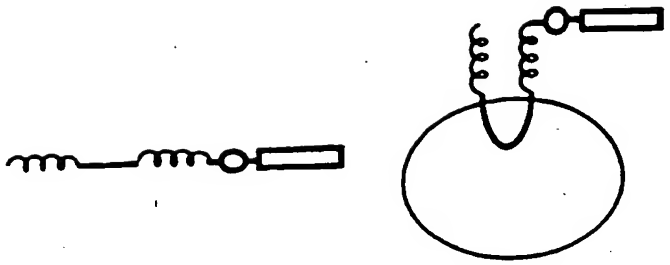

FIG. 1B

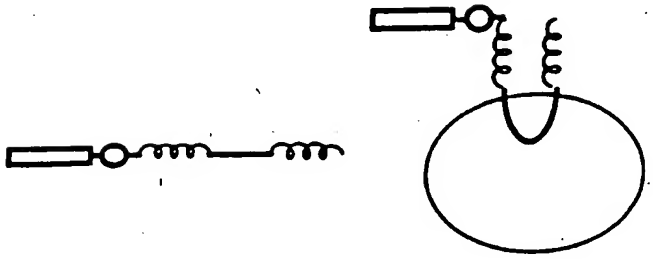

FIG. 1C

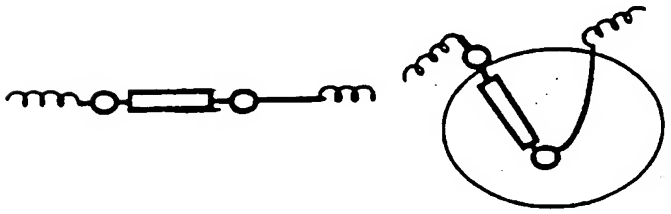

FIG. 1D

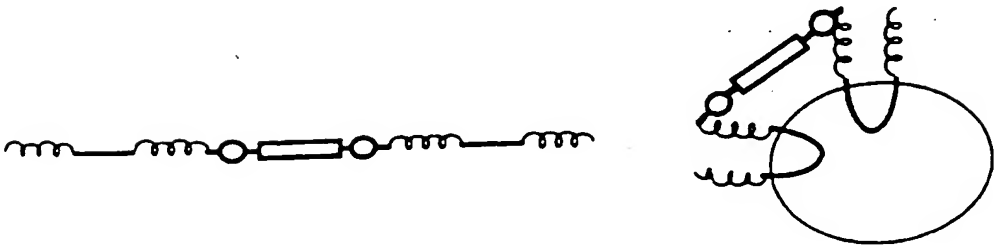

FIGURE 2

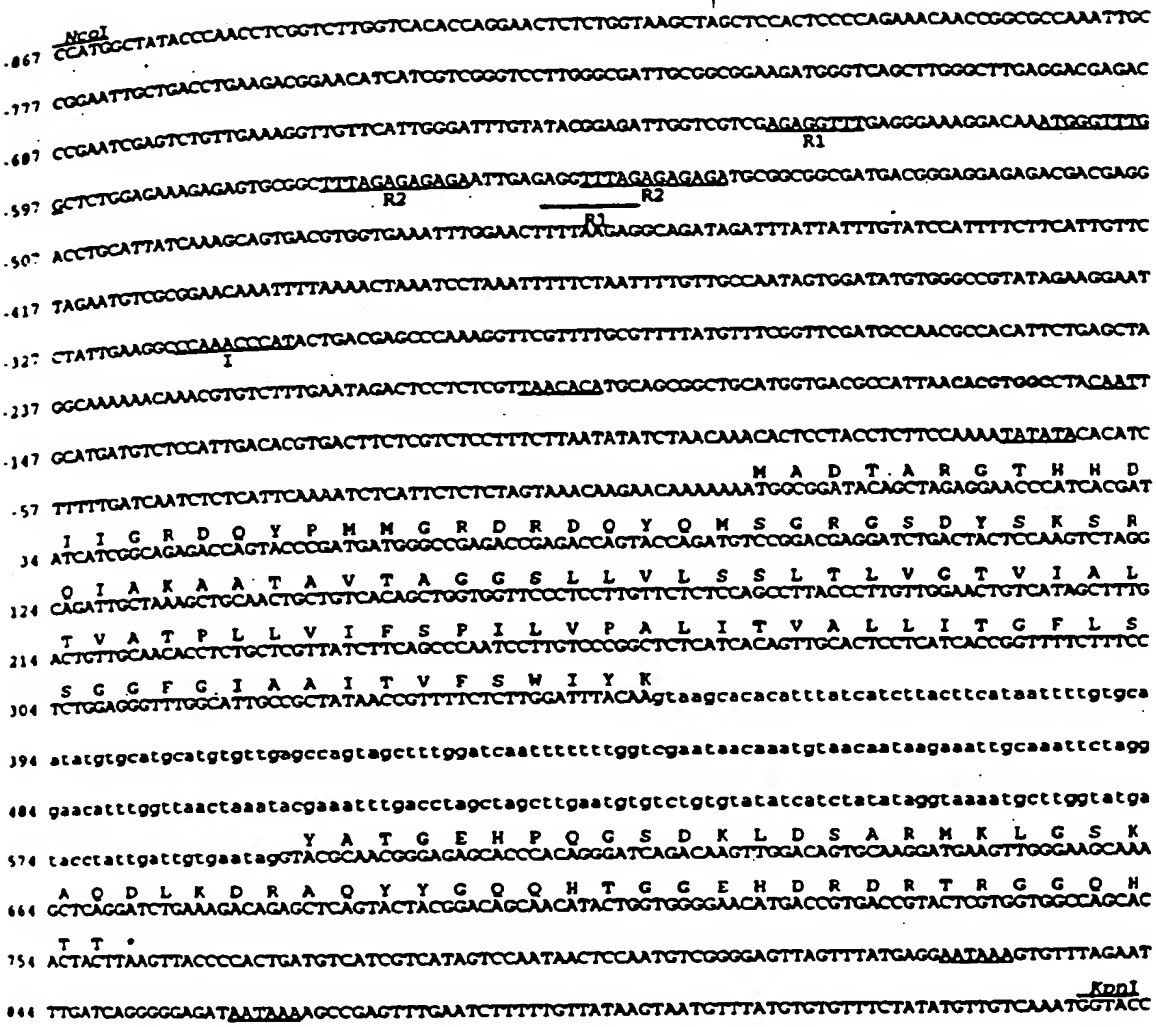
NcoI
R1
R2
R2
R1
I
M A D T A R G T H H D
I I G R D Q Y P M M G R D R D Q Y Q M S G R G S D Y S K S R
Q I A K A A T A V T A G G S L L V L S S L T L V C T V I A L
T V A T P L L V I F S P I L V P A L I T V A L L I T G F L S
S G G F G I A A I T V F S W I Y K
Y A T G E H P Q G S D K L D S A R M K L G S K
A Q D L K D R A Q Y Y G Q Q H T G G E H D R D R T R G G Q H
T T *
KpnI

FIGURE 3

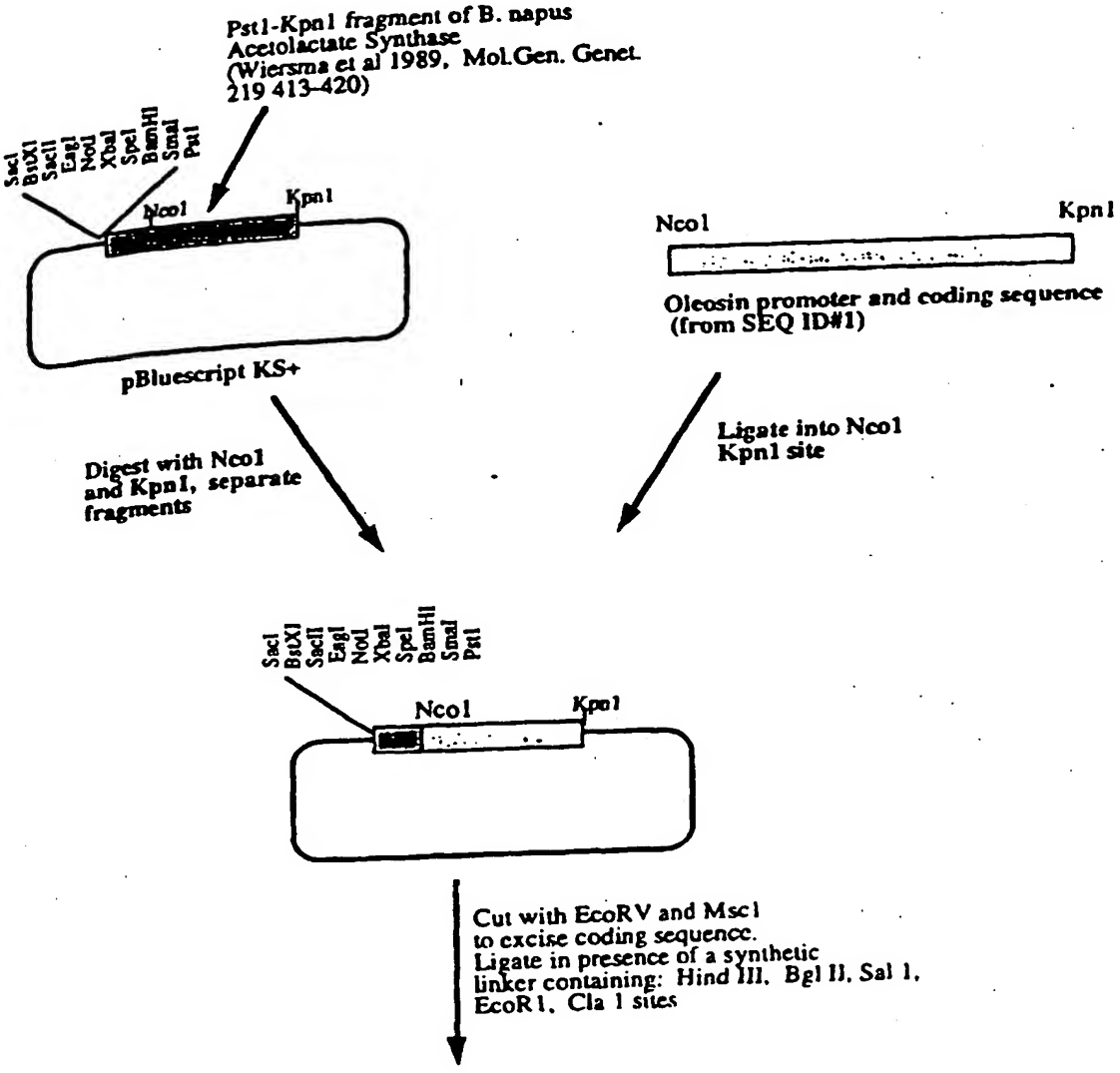
Pst1-Kpn1 fragment of B. napus
Acetolactate Synthase
(Wiersma et al 1989, Mol.Gen. Genet.
219 413-420)
Sac1
BstX1
Sac11
Eag1
Not1
Xba1
Spe1
BamHI
Sma1
Pst1
Nco1
Kpn1
pBluescript KS+
Nco1
Kpn1
Oleosin promoter and coding sequence
(from SEQ ID#1)
Digest with Nco1
and Kpn1, separate
fragments
Ligate into Nco1
Kpn1 site
Sac1
BstX1
Sac11
Eag1
Not1
Xba1
Spe1
BamHI
Sma1
Pst1
Nco1
Kpn1
Cut with EcoRV and Msc1
to excise coding sequence.
Ligate in presence of a synthetic
linker containing: Hind III, Bgl II, Sal 1,
EcoR1, Cla 1 sites

FIGURE 4

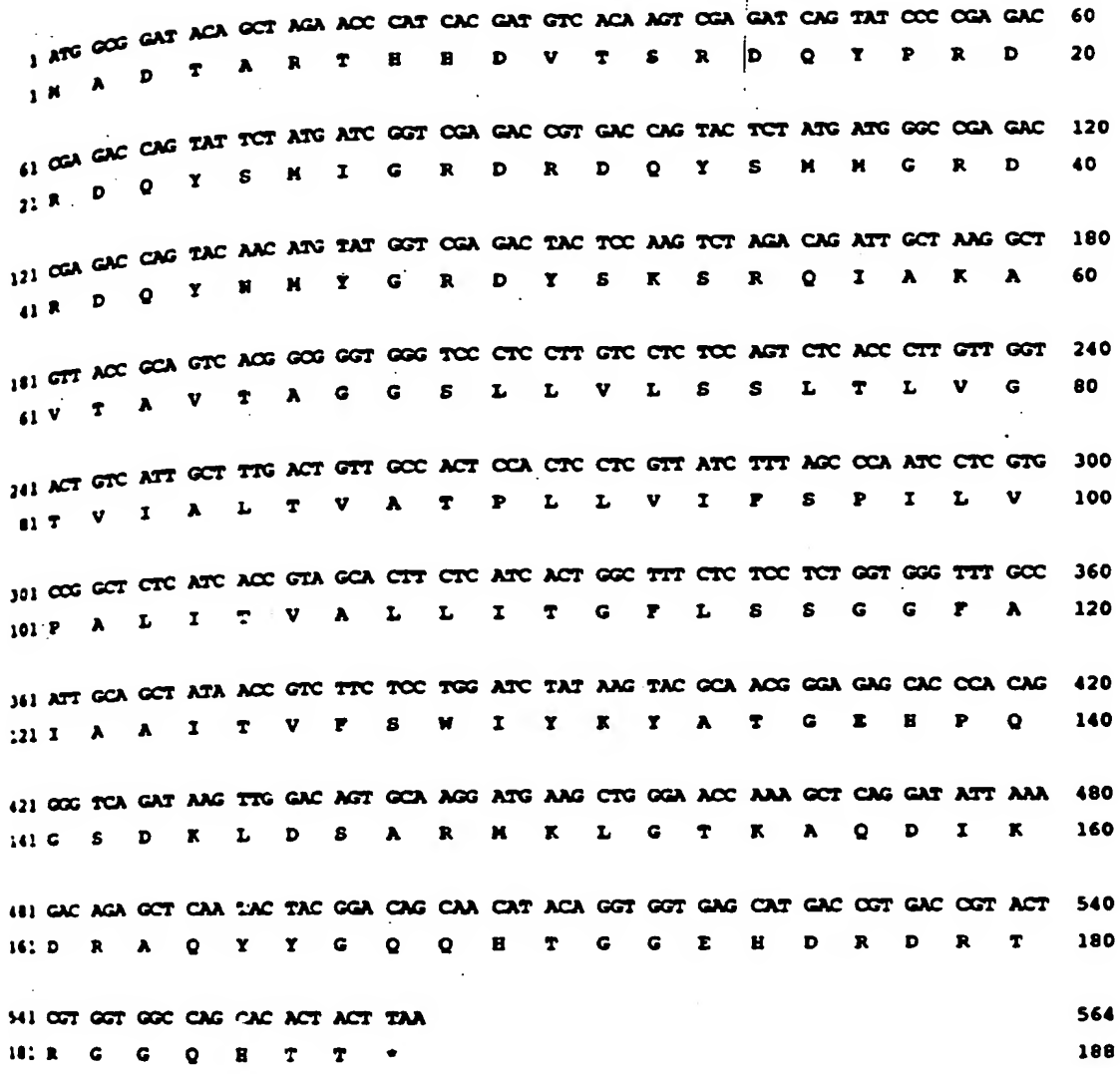
1 ATG GCG GAT ACA GCT AGA ACC CAT CAC GAT GTC ACA AGT CGA GAT CAG TAT CCC CGA GAC 60
1 M A D T A R T H H D V T S R D Q Y P R D 20
61 CGA GAC CAG TAT TCT ATG ATC GGT CGA GAC CGT GAC CAG TAC TCT ATG ATG GGC CGA GAC 120
21 R D Q Y S M I G R D R D Q Y S M M G R D 40
121 CGA GAC CAG TAC AAC ATG TAT GGT CGA GAC TAC TCC AAG TCT AGA CAG ATT GCT AAG GCT 180
41 R D Q Y N M Y G R D Y S K S R Q I A K A 60
181 GTT ACC GCA GTC ACG GCG GGT GGG TCC CTC CTT GTC CTC TCC AGT CTC ACC CTT GTT GGT 240
61 V T A V T A G G S L L V L S S L T L V G 80
241 ACT GTC ATT GCT TTG ACT GTT GCC ACT CCA CTC CTC GTT ATC TTT AGC CCA ATC CTC GTG 300
81 T V I A L T V A T P L L V I F S P I L V 100
301 CCG GCT CTC ATC ACC GTA GCA CTT CTC ATC ACT GGC TTT CTC TCC TCT GGT GGG TTT GCC 360
101 P A L I T V A L L I T G F L S S G G F A 120
361 ATT GCA GCT ATA ACC GTC TTC TCC TGG ATC TAT AAG TAC GCA ACG GGA GAG CAC CCA CAG 420
121 I A A I T V F S W I Y K Y A T G E H P Q 140
421 GGG TCA GAT AAG TTG GAC AGT GCA AGG ATG AAG CTG GGA ACC AAA GCT CAG GAT ATT AAA 480
141 G S D K L D S A R M K L G T K A Q D I K 160
481 GAC AGA GCT CAA TAC TAC GGA CAG CAA CAT ACA GGT GGT GAG CAT GAC CGT GAC CGT ACT 540
161 D R A Q Y Y G Q Q H T G G E H D R D R T 180
541 CGT GGT GGC CAG CAC ACT ACT TAA 564
181 R G G Q H T T * 188

FIGURE 5

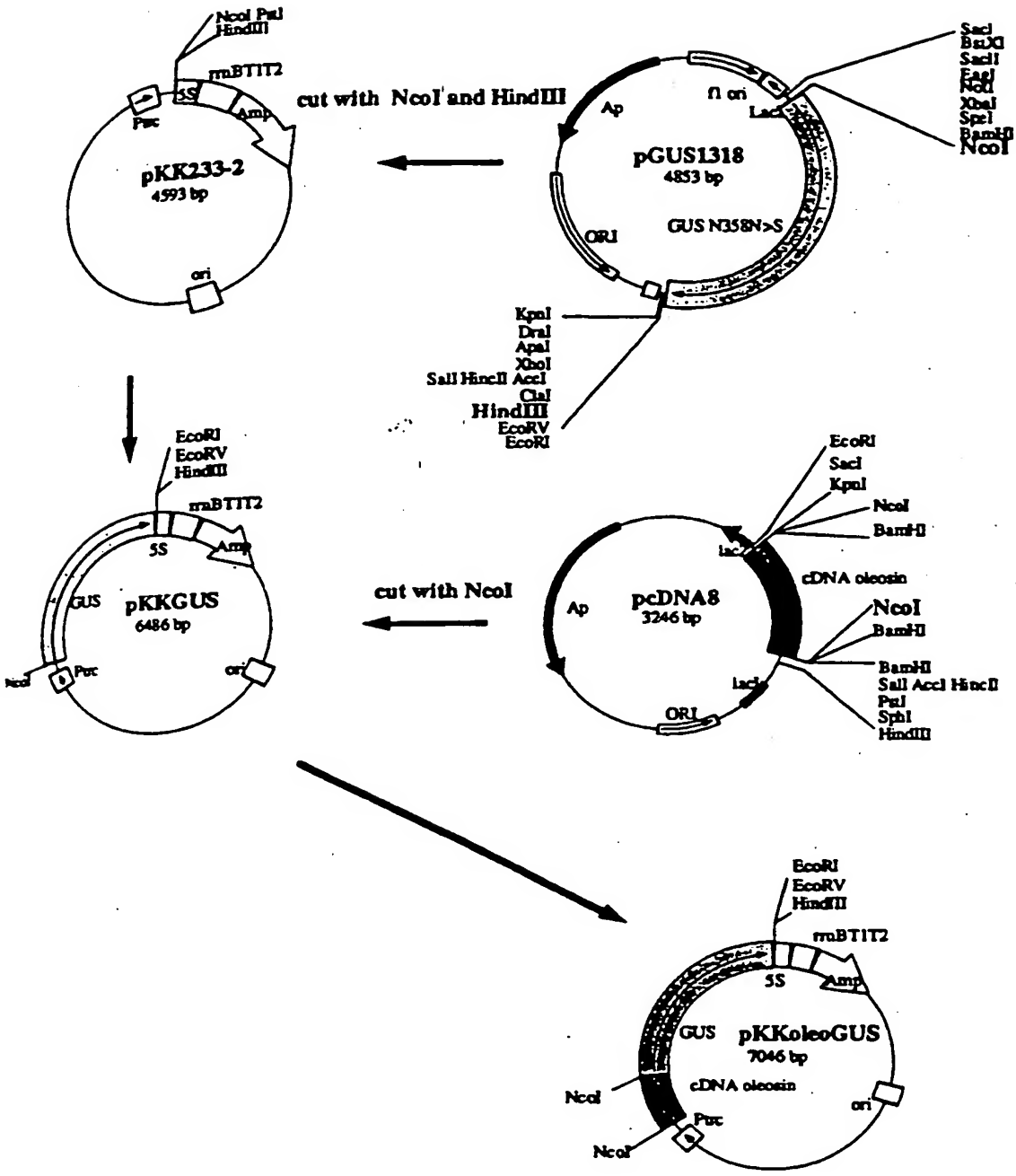
NcoI PstI
HindIII
rrnBT1T2
5S
Amp
Ptac
pKK233-2
4593 bp
ori
cut with NcoI and HindIII
Ap
f1 ori
Lacl
pGUS1318
4853 bp
ORI
GUS N358N>S
SacI
BstXI
SacII
EagI
NotI
XbaI
SpeI
BamHI
NcoI
KpnI
DraI
ApaI
XhoI
SalI HincII AccI
ClaI
HindIII
EcoRV
EcoRI
EcoRI
EcoRV
HindIII
rrnBT1T2
5S
Amp
GUS
pKKGUS
6486 bp
NcoI
Ptac
ori
cut with NcoI
Ap
pcDNA8
3246 bp
lacI
ORI
EcoRI
SacI
KpnI
NcoI
BamHI
cDNA oleosin
NcoI
BamHI
BamHI
SalI AccI HincII
PstI
SphI
HindIII
EcoRI
EcoRV
HindIII
rrnBT1T2
5S
Amp
GUS
pKKoleoGUS
7046 bp
cDNA oleosin
NcoI
Ptac
NcoI
ori

FIGURE 6

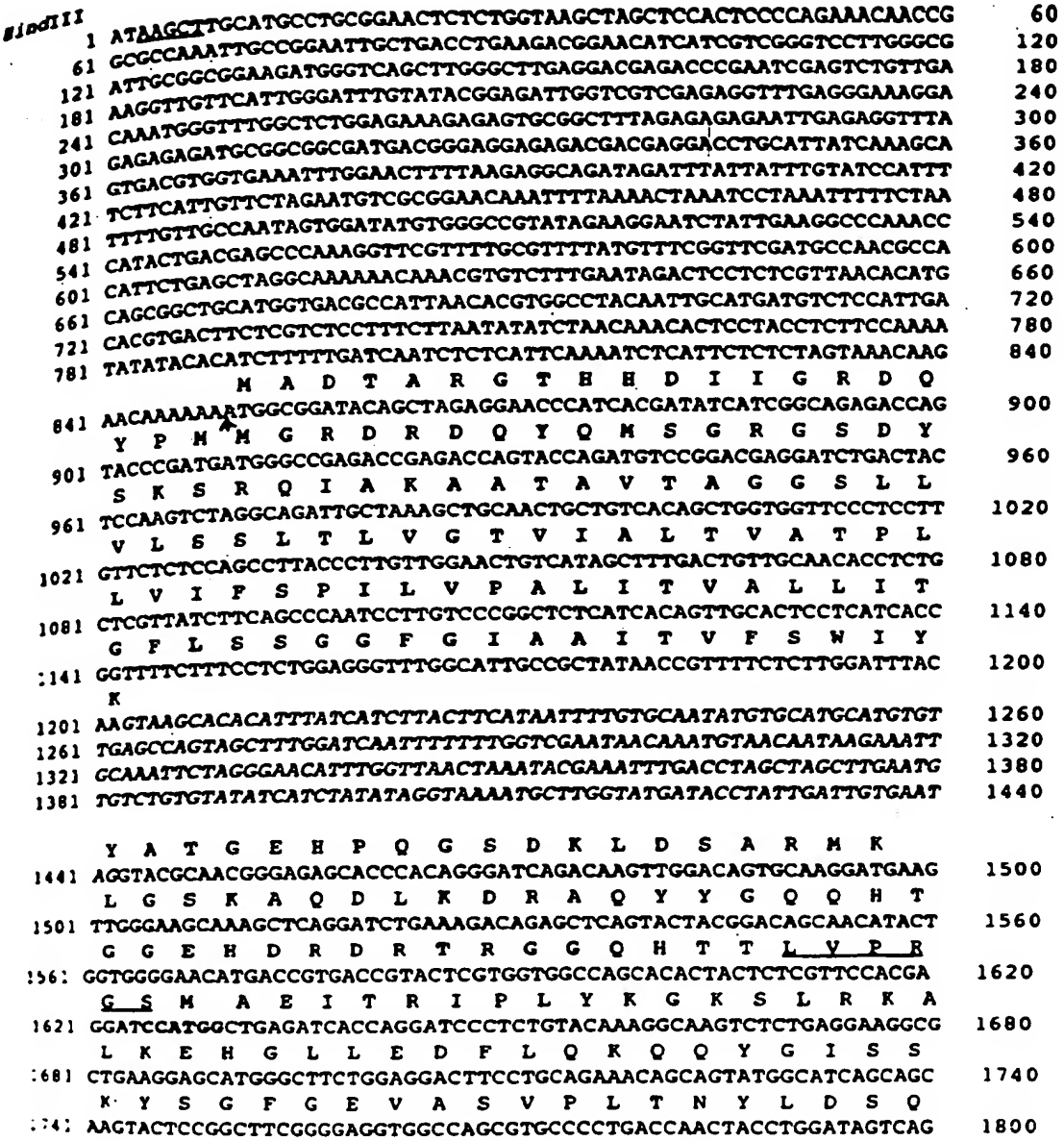
HindIII
1 ATAAGCTTGCATGCCTGCGGAACTCTCTGGTAAGCTAGCTCCACTCCCCAGAAACAACCG 60
61 GCGCCAAATTGCCGGAATTGCTGACCTGAAGACGGAACATCATCGTCGGGTCCTTGGGCG 120
121 ATTGCGGCGGAAGATGGGTCAGCTTGGGCTTGAGGACGAGACCCGAATCGAGTCTGTTGA 180
181 AAGGTTGTTCATTGGGATTTGTATACGGAGATTGGTCGTCGAGAGGTTTGAGGGAAAGGA 240
241 CAAATGGGTTTGGCTCTGGAGAAAGAGAGTGCGGCTTTAGAGAGAGAATTGAGAGGTTTA 300
301 GAGAGAGATGCGGCGGCGATGACGGGAGGAGAGACGACGAGGACCTGCATTATCAAAGCA 360
361 GTGACGTGGTGAAATTTGGAACTTTTAAGAGGCAGATAGATTTATTATTTGTATCCATTT 420
421 TCTTCATTGTTCTAGAATGTCGCGGAACAAATTTTAAAACTAAATCCTAAATTTTTCTAA 480
481 TTTTGTTGCCAATAGTGGATATGTGGGCCGTATAGAAGGAATCTATTGAAGGCCCAAACC 540
541 CATACTGACGAGCCCAAAGGTTCGTTTTGCGTTTTATGTTTCGGTTCGATGCCAACGCCA 600
601 CATTCTGAGCTAGGCAAAAAACAAACGTGTCTTTGAATAGACTCCTCTCGTTAACACATG 660
661 CAGCGGCTGCATGGTGACGCCATTAACACGTGGCCTACAATTGCATGATGTCTCCATTGA 720
721 CACGTGACTTCTCGTCTCCTTTCTTAATATATCTAACAAACACTCCTACCTCTTCCAAAA 780
781 TATATACACATCTTTTTGATCAATCTCTCATTCAAAATCTCATTCTCTCTAGTAAACAAG 840
M A D T A R G T H H D I I G R D Q
841 AACAAAAAAATGGCGGATACAGCTAGAGGAACCCATCACGATATCATCGGCAGAGACCAG 900
Y P M M G R D R D Q Y Q M S G R G S D Y
901 TACCCGATGATGGGCCGAGACCGAGACCAGTACCAGATGTCCGGACGAGGATCTGACTAC 960
S K S R Q I A K A A T A V T A G G S L L
961 TCCAAGTCTAGGCAGATTGCTAAAGCTGCAACTGCTGTCACAGCTGGTGGTTCCCTCCTT 1020
V L S S L T L V G T V I A L T V A T P L
1021 GTTCTCTCCAGCCTTACCCTTGTTGGAACTGTCATAGCTTTGACTGTTGCAACACCTCTG 1080
L V I F S P I L V P A L I T V A L L I T
1081 CTCGTTATCTTCAGCCCAATCCTTGTCCCGGCTCTCATCACAGTTGCACTCCTCATCACC 1140
G F L S S G G F G I A A I T V F S W I Y
1141 GGTTTTCTTTCCTCTGGAGGGTTTGGCATTGCCGCTATAACCGTTTTCTCTTGGATTTAC 1200
K
1201 AAGTAAGCACACATTTATCATCTTACTTCATAATTTTGTGCAATATGTGCATGCATGTGT 1260
1261 TGAGCCAGTAGCTTTGGATCAATTTTTTTGGTCGAATAACAAATGTAACAATAAGAAATT 1320
1321 GCAAATTCTAGGGAACATTTGGTTAACTAAATACGAAATTTGACCTAGCTAGCTTGAATG 1380
1381 TGTCTGTGTATATCATCTATATAGGTAAAATGCTTGGTATGATACCTATTGATTGTGAAT 1440
Y A T G E H P Q G S D K L D S A R M K
1441 AGGTACGCAACGGGAGAGCACCCACAGGGATCAGACAAGTTGGACAGTGCAAGGATGAAG 1500
L G S K A Q D L K D R A Q Y Y G Q Q H T
1501 TTGGGAAGCAAAGCTCAGGATCTGAAAGACAGAGCTCAGTACTACGGACAGCAACATACT 1560
G G E H D R D R T R G G Q H T T L V P R
1561 GGTGGGGAACATGACCGTGACCGTACTCGTGGTGGCCAGCACACTACTCTCGTTCCACGA 1620
G S M A E I T R I P L Y K G K S L R K A
1621 GGATCCATGGCTGAGATCACCAGGATCCCTCTGTACAAAGGCAAGTCTCTGAGGAAGGCG 1680
L K E H G L L E D F L Q K Q Q Y G I S S
1681 CTGAAGGAGCATGGGCTTCTGGAGGACTTCCTGCAGAAACAGCAGTATGGCATCAGCAGC 1740
K Y S G F G E V A S V P L T N Y L D S Q
1741 AAGTACTCCGGCTTCGGGGAGGTGGCCAGCGTGCCCCTGACCAACTACCTGGATAGTCAG 1800

FIGURE 6 cont'd

```
      Y  F  G  K  I  Y  L  G  T  P  P  Q  E  F  T  V  L  F  D  T
1801  TACTTTGGGAAGATCTACCTCGGGACCCCGCCCCAGGAGTTCACCGTGCTGTTTGACACT   1860
      G  S  S  D  F  W  V  P  S  I  Y  C  K  S  N  A  C  K  N  H
1861  GGCTCCTCTGACTTCTGGGTACCCTCTATCTACTGCAAGAGCAATGCCTGCAAAAACCAC   1920
      Q  R  F  D  P  R  K  S  S  T  F  Q  N  L  G  K  P  L  S  I
1921  CAGCGCTTCGACCCGAGAAAGTCGTCCACCTTCCAGAACCTGGGCAAGCCCCTGTCTATC   1980
      H  Y  G  T  G  S  M  Q  G  I  L  G  Y  D  T  V  T  V  S  N
1981  CACTACGGGACAGGCAGCATGCAGGGCATCCTGGGCTATGACACCGTCACTGTCTCCAAC   2040
      I  V  D  I  Q  Q  T  V  G  L  S  T  Q  E  P  G  D  V  F  T
2041  ATTGTGGACATCCAGCAGACAGTAGGCCTGAGCACCCAGGAGCCCGGGGACGTCTTCACC   2100
      Y  A  E  F  D  G  I  L  G  M  A  Y  P  S  L  A  S  E  Y  S
2101  TATGCCGAATTCGACGGGATCCTGGGGATGGCCTACCCCTCGCTCGCCTCAGAGTACTCG   2160
      I  P  V  F  D  N  M  M  N  R  H  L  V  A  Q  D  L  F  S  V
2161  ATACCCGTGTTTGACAACATGATGAACAGGCACCTGGTGGCCCAAGACCTGTTCTCGGTT   2220
      Y  M  D  R  N  G  Q  E  S  M  L  T  L  G  A  I  D  P  S  Y
2221  TACATGGACAGGAATGGCCAGGAGAGCATGCTCACGCTGGGGGCCATCGACCCGTCCTAC   2280
      Y  T  G  S  L  H  W  V  P  V  T  V  Q  Q  Y  W  Q  F  T  V
2281  TACACAGGGTCCCTGCACTGGGTGCCCGTGACAGTGCAGCAGTACTGGCAGTTCACTGTG   2340
      D  S  V  T  I  S  G  V  V  V  A  C  E  G  G  C  Q  A  I  L
2341  GACAGTGTCACCATCAGCGGTGTGGTTGTGGCCTGTGAGGGTGGCTGTCAGGCCATCTTG   2400
      D  T  G  T  S  K  L  V  G  P  S  S  D  I  L  N  I  Q  Q  A
2401  GACACGGGCACCTCCAAGCTGGTCGGGCCCAGCAGCGACATCCTCAACATCCAGCAGGCC   2460
      I  G  A  T  Q  N  Q  Y  G  E  F  D  I  D  C  D  N  L  S  Y
2461  ATTGGAGCCACACAGAACCAGTACGGTGAGTTTGACATCGACTGCGACAACCTGAGCTAC   2520
      M  P  T  V  V  P  E  I  N  G  K  M  Y  P  L  T  P  S  A  Y
2521  ATGCCCACTGTGGTCTTTGAGATCAATGGCAAAATGTACCCACTGACCCCCTCCGCCTAT   2580
      T  S  Q  D  Q  G  F  C  T  S  G  F  Q  S  E  N  H  S  Q  K
2581  ACCAGCCAAGACCAGGGCTTCTGTACCAGTGGCTTCCAGAGTGAAAATCATTCCCAGAAA   2640
      W  I  L  G  D  V  F  I  R  E  Y  Y  S  V  F  D  R  A  N  N
2641  TGGATCCTGGGGGATGTTTTCATCCGAGAGTATTACAGCGTCTTTGACAGGGCCAACAAC   2700
      L  V  G  L  A  K  A  I  *
2701  CTCGTGGGGCTGGCCAAAGCCATCTGAAAGCTT                              2733
                                  HindIII
```

FIGURE 7

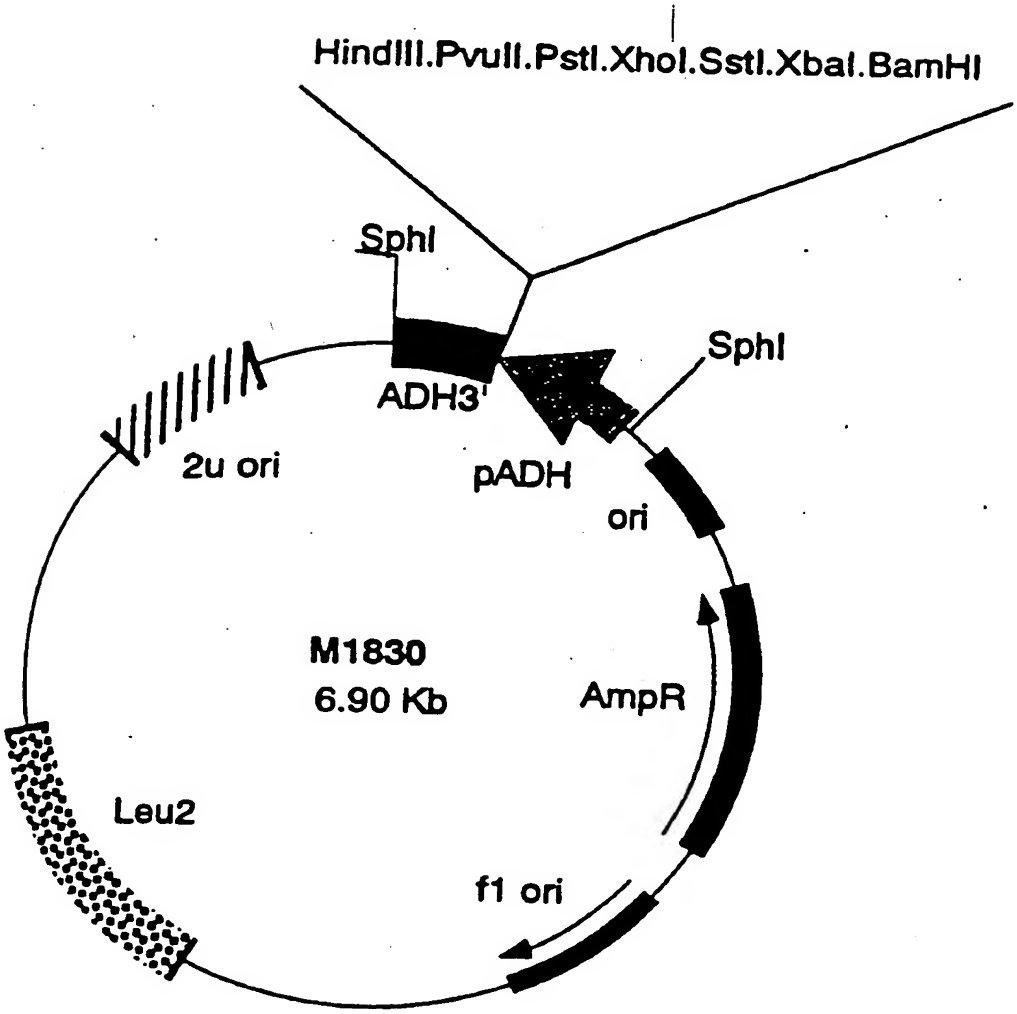
HindIII.PvuII.PstI.XhoI.SstI.XbaI.BamHI
SphI
SphI
ADH3'
2u ori
pADH
ori
M1830
6.90 Kb
AmpR
Leu2
f1 ori

FIGURE 8

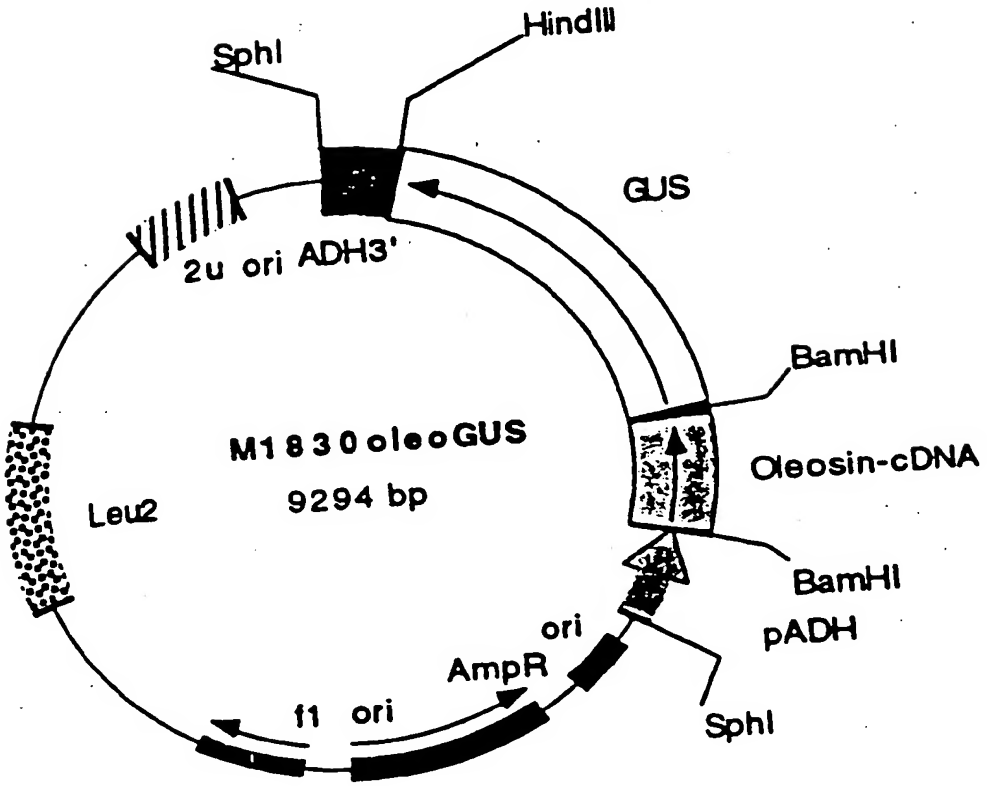
SphI
HindIII
GUS
2u ori ADH3'
BamHI
M1830oleoGUS
9294 bp
Oleosin-cDNA
Leu2
BamHI
pADH
ori
AmpR
f1 ori
SphI

FIGURE 9

Sequence alignment of the isolated caleosin (this application) with the coding sequence of the reported caleosin gene (accession number AF067857). Indicated are the primers GVR979 and GVR980 used for the polymerase Chain Reaction and the one nucleotide change (position 69).

ClustalW Formatted Alignments

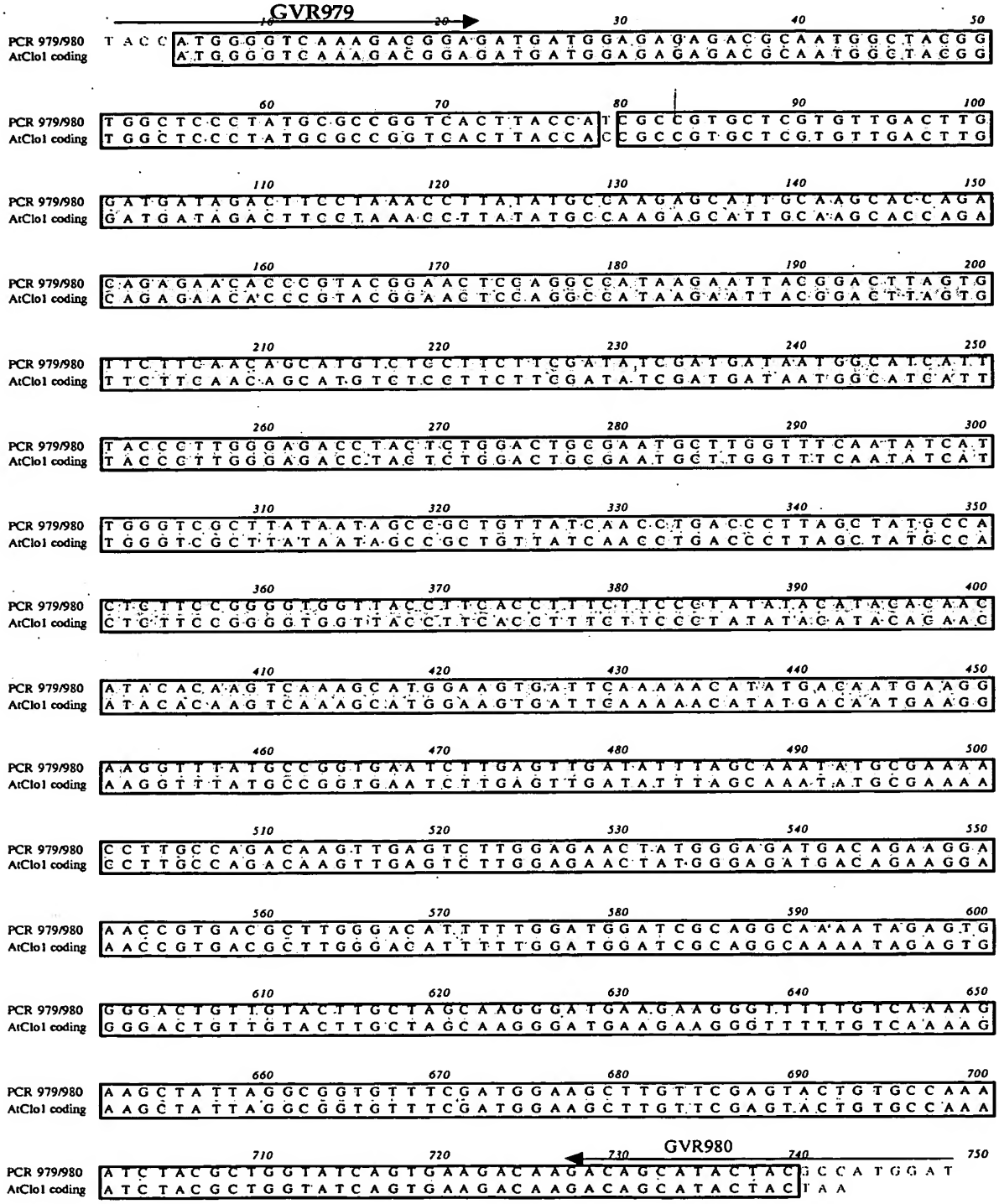

FIGURE 10

Nucleotide sequence of insert of pSBS2098 containing the phaseolin promoter-ß Glucuronidase (GUS)-phaseolin terminator sequence. The GUS sequence and its deduced amino acid sequence is indicated in uppercase. The phaseolin promoter corresponds to nucleotide 1-1547, and the phaseolin terminator corresponds to nucleotide sequence 3426-4646. The terminator was furnished with a a KpnI site (nt 4647-4652) to facilitate cloning.

```
     EcoRI
   1 gaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggtttttacctctatttaaagggg  80
  81 ttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaattatcac 160
 161 gcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaattttatgaagtcccgtct 240
 241 atctttaatgtagtctaacattttcatattgaaatatataatttacttaattttagcgttggtagaaagcataaagattt 320
 321 attcttattcttcttcatataaatgtttaatatacaatataaacaaattctttaccttaagaaggatttcccattttata 400
 401 ttttaaaaatatatttatcaaatatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataaaattta 480
 481 actccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccatttttttctttgaataaaaaa 560
 561 atccaattatcattgtatttttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaagtcatg 640
 641 ttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacatcttcta 720
 721 aagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaattagat 800
 801 ataattaaaatattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactatgtttaa 880
 881 attgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaactataac 960
 961 atttatggtggactaattttcatatatttcttattgcttttacctttttcttggtatgtaagtccgtaactagaattacag 1040
1041 tgggttgccatgacactctgtggtcttttggttcatgcatgggtcttgcgcaagaaaaagacaaagaacaaagaaaaaag 1120
1121 acaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtccatgtat 1200
1201 gtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaacccacacacaaacacat 1280
1281 tgccttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcacttcaacaca 1360
1361 cgtcaacctgcatatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatataataccta 1440
1441 taaatacctctaatatcactcacttctttcatcatccatccatccagagtactactactctactactataataccccaac 1520
1521 ccaactcatattcaatactactctaCC ATG GTC TTA CGT CCT GTA GAA ACC CCA ACC CGT GAA ATC  1586
   1                            M   V   L   R   P   V   E   T   P   T   R   E   I    13
1587 AAA AAA CTC GAC GGC CTG TGG GCA TTC AGT CTG GAT CGC GAA AAC TGT GGA ATT GAT CAG  1646
  14 K   K   L   D   G   L   W   A   F   S   L   D   R   E   N   C   G   I   D   Q    33
1647 CGT TGG TGG GAA AGC GCG TTA CAA GAA AGC CGG GCA ATT GCT GTG CCA GGC AGT TTT AAC  1706
  34 R   W   W   E   S   A   L   Q   E   S   R   A   I   A   V   P   G   S   F   N    53
1707 GAT CAG TTC GCC GAT GCA GAT ATT CGT AAT TAT GCG GGC AAC GTC TGG TAT CAG CGC GAA  1766
  54 D   Q   F   A   D   A   D   I   R   N   Y   A   G   N   V   W   Y   Q   R   E    73
1767 GTC TTT ATA CCG AAA GGT TGG GCA GGC CAG CGT ATC GTG CTG CGT TTC GAT GCG GTC ACT  1826
  74 V   F   I   P   K   G   W   A   G   Q   R   I   V   L   R   F   D   A   V   T    93
1827 CAT TAC GGC AAA GTG TGG GTC AAT AAT CAG GAA GTG ATG GAG CAT CAG GGC GGC TAT ACG  1886
  94 H   Y   G   K   V   W   V   N   N   Q   E   V   M   E   H   Q   G   G   Y   T   113
1887 CCA TTT GAA GCC GAT GTC ACG CCG TAT GTT ATT GCC GGG AAA AGT GTA CGT ATC ACC GTT  1946
 114 P   F   E   A   D   V   T   P   Y   V   I   A   G   K   S   V   R   I   T   V   133
1947 TGT GTG AAC AAC GAA CTG AAC TGG CAG ACT ATC CCG CCG GGA ATG GTG ATT ACC GAC GAA  2006
 134 C   V   N   N   E   L   N   W   Q   T   I   P   P   G   M   V   I   T   D   E   153
2007 AAC GGC AAG AAA AAG CAG TCT TAC TTC CAT GAT TTC TTT AAC TAT GCC GGA ATC CAT CGC  2066
 154 N   G   K   K   K   Q   S   Y   F   H   D   F   F   N   Y   A   G   I   H   R   173
2067 AGC GTA ATG CTC TAC ACC ACG CCG AAC ACC TGG GTG GAC GAT ATC ACC GTG GTG ACG CAT  2126
 174 S   V   M   L   Y   T   T   P   N   T   W   V   D   D   I   T   V   V   T   H   193
2127 GTC GCG CAA GAC TGT AAC CAC GCG TCT GTT GAC TGG CAG GTG GTG GCC AAT GGT GAT GTC  2186
 194 V   A   Q   D   C   N   H   A   S   V   D   W   Q   V   V   A   N   G   D   V   213
2187 AGC GTT GAA CTG CGT GAT GCG GAT CAA CAG GTG GTT GCA ACT GGA CAA GGC ACT AGC GGG  2246
 214 S   V   E   L   R   D   A   D   Q   Q   V   V   A   T   G   Q   G   T   S   G   233
```

FIGURE 10 (cont'd)

```
2247 ACT TTG CAA GTG GTG AAT CCG CAC CTC TGG CAA CCG GGT GAA GGT TAT CTC TAT GAA CTG  2306
 234 T   L   Q   V   V   N   P   H   L   W   Q   P   G   E   G   Y   L   Y   E   L    253
2307 TGC GTC ACA GCC AAA AGC CAG ACA GAG TGT GAT ATC TAC CCG CTT CGC GTC GGC ATC CGG  2366
 254 C   V   T   A   K   S   Q   T   E   C   D   I   Y   P   L   R   V   G   I   R    273

2367 TCA GTG GCA GTG AAG GGC CAA CAG TTC CTG ATT AAC CAC AAA CCG TTC TAC TTT ACT GGC  2426
 274 S   V   A   V   K   G   Q   Q   F   L   I   N   H   K   P   F   Y   F   T   G    293
2427 TTT GGT CGT CAT GAA GAT GCG GAC TTA CGT GGC AAA GGA TTC GAT AAC GTG CTG ATG GTG  2486
 294 F   G   R   H   E   D   A   D   L   R   G   K   G   F   D   N   V   L   M   V    313
2487 CAC GAC CAC GCA TTA ATG GAC TGG ATT GGG GCC AAC TCC TAC CGT ACC TCG CAT TAC CCT  2546
 314 H   D   H   A   L   M   D   W   I   G   A   N   S   Y   R   T   S   H   Y   P    333
2547 TAC GCT GAA GAG ATG CTC GAC TGG GCA GAT GAA CAT GGC ATC GTG GTG ATT GAT GAA ACT  2606
 334 Y   A   E   E   M   L   D   W   A   D   E   H   G   I   V   V   I   D   E   T    353
2607 GCT GCT GTC GGC TTT TCG CTC TCT TTA GGC ATT GGT TTC GAA GCG GGC AAC AAG CCG AAA  2666
 354 A   A   V   G   F   S   L   S   L   G   I   G   F   E   A   G   N   K   P   K    373
2667 GAA CTG TAC AGC GAA GAG GCA GTC AAC GGG GAA ACT CAG CAA GCG CAC TTA CAG GCG ATT  2726
 374 E   L   Y   S   E   E   A   V   N   G   E   T   Q   Q   A   H   L   Q   A   I    393
2727 AAA GAG CTG ATA GCG CGT GAC AAA AAC CAC CCA AGC GTG GTG ATG TGG AGT ATT GCC AAC  2786
 394 K   E   L   I   A   R   D   K   N   H   P   S   V   V   M   W   S   I   A   N    413
2787 GAA CCG GAT ACC CGT CCG CAA GGT GCA CGG GAA TAT TTC GCG CCA CTG GCG GAA GCA ACG  2846
 414 E   P   D   T   R   P   Q   G   A   R   E   Y   F   A   P   L   A   E   A   T    433
2847 CGT AAA CTC GAC CCG ACG CGT CCG ATC ACC TGC GTC AAT GTA ATG TTC TGC GAC GCT CAC  2906
 434 R   K   L   D   P   T   R   P   I   T   C   V   N   V   M   F   C   D   A   H    453
2907 ACC GAT ACC ATC AGC GAT CTC TTT GAT GTG CTG TGC CTG AAC CGT TAT TAC GGA TGG TAT  2966
 454 T   D   T   I   S   D   L   F   D   V   L   C   L   N   R   Y   Y   G   W   Y    473
2967 GTC CAA AGC GGC GAT TTG GAA ACG GCA GAG AAG GTA CTG GAA AAA GAA CTT CTG GCC TGG  3026
 474 V   Q   S   G   D   L   E   T   A   E   K   V   L   E   K   E   L   L   A   W    493
3027 CAG GAG AAA CTG CAT CAG CCG ATT ATC ATC ACC GAA TAC GGC GTG GAT ACG TTA GCC GGG  3086
 494 Q   E   K   L   H   Q   P   I   I   I   T   E   Y   G   V   D   T   L   A   G    513
3087 CTG CAC TCA ATG TAC ACC GAC ATG TGG AGT GAA GAG TAT CAG TGT GCA TGG CTG GAT ATG  3146
 514 L   H   S   M   Y   T   D   M   W   S   E   E   Y   Q   C   A   W   L   D   M    533
3147 TAT CAC CGC GTC TTT GAT CGC GTC AGC GCC GTC GTC GGT GAA CAG GTA TGG AAT TTC GCC  3206
 534 Y   H   R   V   F   D   R   V   S   A   V   V   G   E   Q   V   W   N   F   A    553
3207 GAT TTT GCG ACC TCG CAA GGC ATA TTG CGC GTT GGC GGT AAC AAG AAA GGG ATC TTC ACT  3266
 554 D   F   A   T   S   Q   G   I   L   R   V   G   G   N   K   K   G   I   F   T    573
3267 CGC GAC CGC AAA CCG AAG TCG GCG GCT TTT CTG CTG CAA AAA CGC TGG ACT GGC ATG AAC  3326
 574 R   D   R   K   P   K   S   A   A   F   L   L   Q   K   R   W   T   G   M   N    593
3327 TTC GGT GAA AAA CCG CAG CAG GGA GGC AAA CAA TGA ATCAACAACTCTCCTGGCGCACCATCGTCGGC 3394
 594 F   G   E   K   P   Q   Q   G   G   K   Q   *                                    605
3395 TACAGCCTCGGTGGAATTCGATATCAAGCTTaaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagc 3474
3475 atggaatattgtatccgaccatgtaacagtataataactgagctccatctcacttcttctatgaataaacaaaggatgtt 3554
3555 atgatatattaacactctatctatgcaccttattgttctatgataaatttcctcttattattataaatcatctgaatcgt 3634
3635 gacggcttatggaatgcttcaaatagtacaaaaacaaatgtgtactataagactttctaaacaattctaactttagcatt 3714
3715 gtgaacgagacataagtgttaagaagacataacaattataatggaagaagtttgtctccatttatatattatatattacc 3794
3795 cacttatgtattatattaggatgttaaggagacataacaattataaagagagaagtttgtatccatttatatattatata 3874
3875 ctacccatttatatattatacttatccacttatttaatgtctttataaggtttgatccatgatatttctaatattttagt 3954
3955 tgatatgtatatgaaagggtactatttgaactctcttactctgtataaaggttggatcatccttaaagtgggtctattta 4034
4035 attttattgcttcttacagataaaaaaaaaattatgagttggtttgataaaatattgaaggatttaaaataataataaat 4114
4115 aataaataacatataatatatgtatataaatttattataatataacatttatctataaaaaagtaaatattgtcataaat 4194
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FIGURE 10 (cont'd)

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4195 ctatacaatcgtttagccttgctggacgactctcaattatttaaacgagagtaaacatatttgacttttggttatttaa 4274
4275 caaattattatttaacactatatgaaatttttttttttatcggcaaggaaataaaattaaattaggagggacaatggtg 4354
4355 tgtcccaatccttatacaaccaacttccacaggaaggtcaggtcggggacaacaaaaaaacaggcaagggaaatttttta 4434
4435 atttgggttgtcttgtttgctgcataatttatgcagtaaaacactacacataaccctttagcagtagagcaatggttga 4514
4515 ccgtgtgcttagcttcttttatttttatttttttatcagcaaagaataaataaaataaaatgagacacttcagggatgttt 4594
4595 caacccttatacaaaaccccaaaaacaagtttcctagcaccctaccaactaaGGTACC                       4652
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FIGURE 11

Nucleotide sequence of the phaseolin promoter-oleosinGUS-phaseolin terminator sequence. The oleosinGUS coding sequence and its deduced aminoacid sequence is indicated. The phaseolin promoter corresponds to nucleotide 6-1554. The sequence encoding oleosin corresponds to nt 1555-2313, the intron in this sequence (nt 1908-2147) is indicated in italics. The GUS sequence corresponds to nt 2314-4191. The phaseolin terminator corresponds to nucleotide sequence 4192-5412.

```
     PstI   EcoRI
   1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggtttttttacctctattta  80
  81 aaggggttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaat 160
 161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaatttttatgaagtc 240
 241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaattttagcgttggtagaaagcataa 320
 321 tgatttattcttattcttcttcatataaatgtttaatatacaatataaacaaattctttaccttaagaaggatttcccat 400
 401 tttatattttaaaaatatatttatcaaatatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480
 481 aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccatttttttctttgaat 560
 561 aaaaaaatccaattatcattgtatttttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaa 640
 641 gtcatgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720
 721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800
 801 ttagatataattaaaatattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat 880
 881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaac 960
 961 tataagatttatggtggactaattttcatatatttcttattgcttttacctttttcttggtatgtaagtccgtaactggaa 1040
1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120
1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200
1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaacccacacaca 1280
1281 aacacattgccttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360
1361 caacacacgtcaacctgcatatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatata 1440
1441 atacctataaataacctctaatatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520
1521 ccccaacccaactcatattcaatactactctact ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT   1587
   1                                    M   A   D   T   A   R   G   T   H   H   D     11
1588 ATC ATC GGC AGA GAC CAG TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC  1647
  12 I   I   G   R   D   Q   Y   P   M   M   G   R   D   R   D   Q   Y   Q   M   S    31
1648 GGA CGA GGA TCT GAC TAC TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA  1707
  32 G   R   G   S   D   Y   S   K   S   R   Q   I   A   K   A   A   T   A   V   T    51
1708 GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG  1767
  52 A   G   G   S   L   L   V   L   S   S   L   T   L   V   G   T   V   I   A   L    71
1768 ACT GTT GCA ACA CCT CTG CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA  1827
  72 T   V   A   T   P   L   L   V   I   F   S   P   I   L   V   P   A   L   I   T    91
1828 GTT GCA CTC CTC ATC ACC GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC  1887
  92 V   A   L   L   I   T   G   F   L   S   S   G   G   F   G   I   A   A   I   T   111
1888 GTT TTC TCT TGG ATT TAC AA gtaagcacacatttatcatcttacttcataattttgtgcaatatgtgcatgca 1960
 112 V   F   S   W   I   Y   K                                                       118
1961 tgtgttgagccagtagctttggatcaatttttttggtcgaataacaaatgtaacaataagaaattgcaaattctagggaa 2040
2041 catttggttaactaaatacgaaatttgacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgctt 2120
2121 ggtatgatacctattgattgtgaatag G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG      2184
 119                             Y   A   T   G   E   H   P   Q   G   S   D   K       130
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FIGURE 11 (cont'd)

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2185 TTG GAC AGT GCA AGG ATG AAG TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG 2244
 131 L   D   S   A   R   M   K   L   G   S   K   A   Q   D   L   K   D   R   A   Q  150
2245 TAC TAC GGA CAG CAA CAT ACT GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG 2304
 151 Y   Y   G   Q   Q   H   T   G   G   E   H   D   R   D   R   T   R   G   G   Q  170
2305 CAC ACT ACC ATG GTC TTA CGT CCT GTA GAA ACC CCA ACC CGT GAA ATC AAA AAA CTC GAC 2364
 171 H   T   T   M   V   L   R   P   V   E   T   P   T   R   E   I   K   K   L   D  190
2365 GGC CTG TGG GCA TTC AGT CTG GAT CGC GAA AAC TGT GGA ATT GAT CAG CGT TGG TGG GAA 2424
 191 G   L   W   A   F   S   L   D   R   E   N   C   G   I   D   Q   R   W   W   E  210
2425 AGC GCG TTA CAA GAA AGC CGG GCA ATT GCT GTG CCA GGC AGT TTT AAC GAT CAG TTC GCC 2484
 211 S   A   L   Q   E   S   R   A   I   A   V   P   G   S   F   N   D   Q   F   A  230
2485 GAT GCA GAT ATT CGT AAT TAT GCG GGC AAC GTC TGG TAT CAG CGC GAA GTC TTT ATA CCG 2544
 231 D   A   D   I   R   N   Y   A   G   N   V   W   Y   Q   R   E   V   F   I   P  250
2545 AAA GGT TGG GCA GGC CAG CGT ATC GTG CTG CGT TTC GAT GCG GTC ACT CAT TAC GGC AAA 2604
 251 K   G   W   A   G   Q   R   I   V   L   R   F   D   A   V   T   H   Y   G   K  270
2605 GTG TGG GTC AAT AAT CAG GAA GTG ATG GAG CAT CAG GGC GGC TAT ACG CCA TTT GAA GCC 2664
 271 V   W   V   N   N   Q   E   V   M   E   H   Q   G   G   Y   T   P   F   E   A  290
2665 GAT GTC ACG CCG TAT GTT ATT GCC GGG AAA AGT GTA CGT ATC ACC GTT TGT GTG AAC AAC 2724
 291 D   V   T   P   Y   V   I   A   G   K   S   V   R   I   T   V   C   V   N   N  310
2725 GAA CTG AAC TGG CAG ACT ATC CCG CCG GGA ATG GTG ATT ACC GAC GAA AAC GGC AAG AAA 2784
 311 E   L   N   W   Q   T   I   P   P   G   M   V   I   T   D   E   N   G   K   K  330
2785 AAG CAG TCT TAC TTC CAT GAT TTC TTT AAC TAT GCC GGA ATC CAT CGC AGC GTA ATG CTC 2844
 331 K   Q   S   Y   F   H   D   F   F   N   Y   A   G   I   H   R   S   V   M   L  350
2845 TAC ACC ACG CCG AAC ACC TGG GTG GAC GAT ATC ACC GTG GTG ACG CAT GTC GCG CAA GAC 2904
 351 Y   T   T   P   N   T   W   V   D   D   I   T   V   V   T   H   V   A   Q   D  370
2905 TGT AAC CAC GCG TCT GTT GAC TGG CAG GTG GTG GCC AAT GGT GAT GTC AGC GTT GAA CTG 2964
 371 C   N   H   A   S   V   D   W   Q   V   V   A   N   G   D   V   S   V   E   L  390
2965 CGT GAT GCG GAT CAA CAG GTG GTT GCA ACT GGA CAA GGC ACT AGC GGG ACT TTG CAA GTG 3024
 391 R   D   A   D   Q   Q   V   V   A   T   G   Q   G   T   S   G   T   L   Q   V  410
3025 GTG AAT CCG CAC CTC TGG CAA CCG GGT GAA GGT TAT CTC TAT GAA CTG TGC GTC ACA GCC 3084
 411 V   N   P   H   L   W   Q   P   G   E   G   Y   L   Y   E   L   C   V   T   A  430
3085 AAA AGC CAG ACA GAG TGT GAT ATC TAC CCG CTT CGC GTC GGC ATC CGG TCA GTG GCA GTG 3144
 431 K   S   Q   T   E   C   D   I   Y   P   L   R   V   G   I   R   S   V   A   V  450
3145 AAG GGC CAA CAG TTC CTG ATT AAC CAC AAA CCG TTC TAC TTT ACT GGC TTT GGT CGT CAT 3204
 451 K   G   Q   Q   F   L   I   N   H   K   P   F   Y   F   T   G   F   G   R   H  470
3205 GAA GAT GCG GAC TTA CGT GGC AAA GGA TTC GAT AAC GTG CTG ATG GTG CAC GAC CAC GCA 3264
 471 E   D   A   D   L   R   G   K   G   F   D   N   V   L   M   V   H   D   H   A  490
3265 TTA ATG GAC TGG ATT GGG GCC AAC TCC TAC CGT ACC TCG CAT TAC CCT TAC GCT GAA GAG 3324
 491 L   M   D   W   I   G   A   N   S   Y   R   T   S   H   Y   P   Y   A   E   E  510
3325 ATG CTC GAC TGG GCA GAT GAA CAT GGC ATC GTG GTG ATT GAT GAA ACT GCT GCT GTC GGC 3384
 511 M   L   D   W   A   D   E   H   G   I   V   V   I   D   E   T   A   A   V   G  530
3385 TTT TCG CTC TCT TTA GGC ATT GGT TTC GAA GCG GGC AAC AAG CCG AAA GAA CTG TAC AGC 3444
 531 F   S   L   S   L   G   I   G   F   E   A   G   N   K   P   K   E   L   Y   S  550
3445 GAA GAG GCA GTC AAC GGG GAA ACT CAG CAA GCG CAC TTA CAG GCG ATT AAA GAG CTG ATA 3504
 551 E   E   A   V   N   G   E   T   Q   Q   A   H   L   Q   A   I   K   E   L   I  570
3505 GCG CGT GAC AAA AAC CAC CCA AGC GTG GTG ATG TGG AGT ATT GCC AAC GAA CCG GAT ACC 3564
 571 A   R   D   K   N   H   P   S   V   V   M   W   S   I   A   N   E   P   D   T  590
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FIGURE 11 (cont'd)

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3565 CGT CCG CAA GGT GCA CGG GAA TAT TTC GCG CCA CTG GCG GAA GCA ACG CGT AAA CTC GAC 3624
 591 R   P   Q   G   A   R   E   Y   F   A   P   L   A   E   A   T   R   K   L   D   610
3625 CCG ACG CGT CCG ATC ACC TGC GTC AAT GTA ATG TTC TGC GAC GCT CAC ACC GAT ACC ATC 3684
 611 P   T   R   P   I   T   C   V   N   V   M   F   C   D   A   H   T   D   T   I   630
3685 AGC GAT CTC TTT GAT GTG CTG TGC CTG AAC CGT TAT TAC GGA TGG TAT GTC CAA AGC GGC 3744
 631 S   D   L   F   D   V   L   C   L   N   R   Y   Y   G   W   Y   V   Q   S   G   650
3745 GAT TTG GAA ACG GCA GAG AAG GTA CTG GAA AAA GAA CTT CTG GCC TGG CAG GAG AAA CTG 3804
 651 D   L   E   T   A   E   K   V   L   E   K   E   L   L   A   W   Q   E   K   L   670
3805 CAT CAG CCG ATT ATC ATC ACC GAA TAC GGC GTG GAT ACG TTA GCC GGG CTG CAC TCA ATG 3864
 671 H   Q   P   I   I   I   T   E   Y   G   V   D   T   L   A   G   L   H   S   M   690
3865 TAC ACC GAC ATG TGG AGT GAA GAG TAT CAG TGT GCA TGG CTG GAT ATG TAT CAC CGC GTC 3924
 691 Y   T   D   M   W   S   E   E   Y   Q   C   A   W   L   D   M   Y   H   R   V   710
3925 TTT GAT CGC GTC AGC GCC GTC GTC GGT GAA CAG GTA TGG AAT TTC GCC GAT TTT GCG ACC 3984
 711 F   D   R   V   S   A   V   V   G   E   Q   V   W   N   F   A   D   F   A   T   730
3985 TCG CAA GGC ATA TTG CGC GTT GGC GGT AAC AAG AAA GGG ATC TTC ACT CGC GAC CGC AAA 4044
 731 S   Q   G   I   L   R   V   G   G   N   K   K   G   I   F   T   R   D   R   K   750
4045 CCG AAG TCG GCG GCT TTT CTG CTG CAA AAA CGC TGG ACT GGC ATG AAC TTC GGT GAA AAA 4104
 751 P   K   S   A   A   F   L   L   Q   K   R   W   T   G   M   N   F   G   E   K   770
4105 CCG CAG CAG GGA GGC AAA CAA TGA ATCAACAACTCTCCTGGCGCACCATCGTCGGCTACAGCCTCGGTGGAA 4176
 771 P   Q   Q   G   G   K   Q   *                                                   778
4177 TTCGATATCAAGCTTaaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatcc 4256
4257 gaccatgtaacagtataataactgagctccatctcacttcttctatgaataaacaaaggatgttatgatatattaacact 4336
4337 ctatctatgcaccttattgttctatgataaatttcctcttattattataaatcatctgaatcgtgacggcttatggaatg 4416
4417 cttcaaatagtacaaaaacaaatgtgtactataagactttctaaacaattctaactttagcattgtgaacgagacataag 4496
4497 tgttaagaagacataacaattataatggaagaagtttgtctccatttatatattatatattacccacttatgtattatat 4576
4577 taggatgttaaggagacataacaattataaagagagaagtttgtatccatttatatattatatactacccatttatatat 4656
4657 tatacttatccacttatttaatgtctttataaggtttgatccatgatatttctaatattttagttgatatgtatatgaaa 4736
4737 gggtactatttgaactctcttactctgtataaaggttggatcatccttaaagtgggtctatttaattttattgcttctta 4816
4817 cagataaaaaaaaaaattatgagttggtttgataaaatattgaaggatttaaaataataataaataataaataacatataa 4896
4897 tatatgtatataaatttattataatataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgtttag 4976
4977 ccttgctggacgactctcaattatttaaacgagagtaaacatatttgacttttggttatttaacaaattattatttaac 5056
5057 actatatgaaatttttttttttatcggcaaggaaataaaattaaattaggagggacaatggtgtgtcccaatccttata 5136
5137 caaccaacttccacaggaaggtcaggtcggggacaacaaaaaaacaggcaagggaaatttttaatttgggttgtcttgt 5216
5217 ttgctgcataatttatgcagtaaaacactacacataaccctttagcagtagagcaatggttgaccgtgtgcttagcttc 5296
5297 ttttatttttatttttttatcagcaaagaataaataaaataaaatgagacacttcagggatgtttcaacccttatacaaaa 5376
5377 ccccaaaaacaagtttcctagcaccctaccaactaaGGTACC                                       5418
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KpnI

FIGURE 12

Nucleotide sequence of the phaseolin promoter-caleosinGUS-phaseolin terminator sequence. The caleosinGUS coding sequence and its deduced aminoacid sequence is indicated. The phaseolin promoter corresponds to nucleotide 1-1545. The sequence encoding caleosin corresponds to nt 1548-2282, the NcoI restriction, which was used for the in-frame cloning and which separates the caleosin and GUS sequence (nt 2284-2289) is underlined. The GUS sequence corresponds to nt 2286-4163. The phaseolin terminator corresponds to nucleotide sequence 4164-5384.

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   1 GAATTCattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggtttttacctctatttaaagggg  80
  81 ttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaattatcac 160
 161 gcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaattttatgaagtcccgtct 240
 241 atctttaatgtagtctaacattttcatattgaaatatataatttacttaattttagcgttggtagaaagcataaagattt 320
 321 attcttattcttcttcatataaatgtttaatatacaatataaacaaattctttaccttaagaaggatttcccattttata 400
 401 ttttaaaaatatatttatcaaatatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataaaattta 480
 481 actccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccatttttttctttgaataaaaaa 560
 561 atccaattatcattgtatttttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaagtcatg 640
 641 ttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacatcttcta 720
 721 aagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaattagat 800
 801 ataattaaaatattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactatgtttaa 880
 881 attgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaactataac 960
 961 atttatggtggactaattttcatatatttcttattgcttttacctttttcttggtatgtaagtccgtaactagaattacag 1040
1041 tgggttgccatgacactctgtggtcttttggttcatgcatgggtcttgcgcaagaaaaagacaaagaacaaagaaaaaag 1120
1121 acaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtccatgtat 1200
1201 gtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaacccacacacaaacacat 1280
1281 tgccttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcacttcaacaca 1360
1361 cgtcaacctgcatatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatataatacccta 1440
1441 taaatacctctaatatcactcacttctttcatcatccatccatccagagtactactactctactactataataccccaac 1520
1521 ccaactcatattcaatactactctaCC ATG GGG TCA AAG ACG GAG ATG ATG GAG AGA GAC GCA ATG  1586
   1                            M   G   S   K   T   E   M   M   E   R   D   A   M    13
1587 GCT ACG GTG GCT CCC TAT GCG CCG GTC ACT TAC CAC CGC CGT GCT CGT GTT GAC TTG GAT  1646
  14 A   T   V   A   P   Y   A   P   V   T   Y   H   R   R   A   R   V   D   L   D    33
1647 GAT AGA CTT CCT AAA CCT TAT ATG CCA AGA GCA TTG CAA GCA CCA GAC AGA GAA CAC CCG  1706
  34 D   R   L   P   K   P   Y   M   P   R   A   L   Q   A   P   D   R   E   H   P    53
1707 TAC GGA ACT CCA GGC CAT AAG AAT TAC GGA CTT AGT GTT CTT CAA CAG CAT GTC TCC TTC  1766
  54 Y   G   T   P   G   H   K   N   Y   G   L   S   V   L   Q   Q   H   V   S   F    73
1767 TTC GAT ATC GAT GAT AAT GGC ATC ATT TAC CCT TGG GAG ACC TAC TCT GGA CTG CGA ATG  1826
  74 F   D   I   D   D   N   G   I   I   Y   P   W   E   T   Y   S   G   L   R   M    93
1827 CTT GGT TTC AAT ATC ATT GGG TCG CTT ATA ATA GCC GCT GTT ATC AAC CTG ACC CTT AGC  1886
  94 L   G   F   N   I   I   G   S   L   I   I   A   A   V   I   N   L   T   L   S   113
1887 TAT GCC ACT CTT CCG GGG TGG TTA CCT TCA CCT TTC TTC CCT ATA TAC ATA CAC AAC ATA  1946
 114 Y   A   T   L   P   G   W   L   P   S   P   F   F   P   I   Y   I   H   N   I   133
1947 CAC AAG TCA AAG CAT GGA AGT GAT TCA AAA ACA TAT GAC AAT GAA GGA AGG TTT ATG CCG  2006
 134 H   K   S   K   H   G   S   D   S   K   T   Y   D   N   E   G   R   F   M   P   153
2007 GTG AAT CTT GAG TTG ATA TTT AGC AAA TAT GCG AAA ACC TTG CCA GAC AAG TTG AGT CTT  2066
 154 V   N   L   E   L   I   F   S   K   Y   A   K   T   L   P   D   K   L   S   L   173
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FIGURE 12 (cont'd)

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2067 GGA GAA CTA TGG GAG ATG ACA GAA GGA AAC CGT GAC GCT TGG GAC ATT TTT GGA TGG ATC 2126
 174 G   E   L   W   E   M   T   E   G   N   R   D   A   W   D   I   F   G   W   I   193
2127 GCA GGC AAA ATA GAG TGG GGA CTG TTG TAC TTG CTA GCA AGG GAT GAA GAA GGG TTT TTG 2186
 194 A   G   K   I   E   W   G   L   L   Y   L   L   A   R   D   E   E   G   F   L   213
2187 TCA AAA GAA GCT ATT AGG CGG TGT TTC GAT GGA AGC TTG TTC GAG TAC TGT GCC AAA ATC 2246
 214 S   K   E   A   I   R   R   C   F   D   G   S   L   F   E   Y   C   A   K   I   233
2247 TAC GCT GGT ATC AGT GAA GAC AAG ACA GCA TAC TAC GCC ATG GTC TTA CGT CCT GTA GAA 2306
 234 Y   A   G   I   S   E   D   K   T   A   Y   Y   A   M   V   L   R   P   V   E   253
2307 ACC CCA ACC CGT GAA ATC AAA AAA CTC GAC GGC CTG TGG GCA TTC AGT CTG GAT CGC GAA 2366
 254 T   P   T   R   E   I   K   K   L   D   G   L   W   A   F   S   L   D   R   E   273
2367 AAC TGT GGA ATT GAT CAG CGT TGG TGG GAA AGC GCG TTA CAA GAA AGC CGG GCA ATT GCT 2426
 274 N   C   G   I   D   Q   R   W   W   E   S   A   L   Q   E   S   R   A   I   A   293
2427 GTG CCA GGC AGT TTT AAC GAT CAG TTC GCC GAT GCA GAT ATT CGT AAT TAT GCG GGC AAC 2486
 294 V   P   G   S   F   N   D   Q   F   A   D   A   D   I   R   N   Y   A   G   N   313
2487 GTC TGG TAT CAG CGC GAA GTC TTT ATA CCG AAA GGT TGG GCA GGC CAG CGT ATC GTG CTG 2546
 314 V   W   Y   Q   R   E   V   F   I   P   K   G   W   A   G   Q   R   I   V   L   333
2547 CGT TTC GAT GCG GTC ACT CAT TAC GGC AAA GTG TGG GTC AAT AAT CAG GAA GTG ATG GAG 2606
 334 R   F   D   A   V   T   H   Y   G   K   V   W   V   N   N   Q   E   V   M   E   353
2607 CAT CAG GGC GGC TAT ACG CCA TTT GAA GCC GAT GTC ACG CCG TAT GTT ATT GCC GGG AAA 2666
 354 H   Q   G   G   Y   T   P   F   E   A   D   V   T   P   Y   V   I   A   G   K   373
2667 AGT GTA CGT ATC ACC GTT TGT GTG AAC AAC GAA CTG AAC TGG CAG ACT ATC CCG CCG GGA 2726
 374 S   V   R   I   T   V   C   V   N   N   E   L   N   W   Q   T   I   P   P   G   393
2727 ATG GTG ATT ACC GAC GAA AAC GGC AAG AAA AAG CAG TCT TAC TTC CAT GAT TTC TTT AAC 2786
 394 M   V   I   T   D   E   N   G   K   K   K   Q   S   Y   F   H   D   F   F   N   413
2787 TAT GCC GGA ATC CAT CGC AGC GTA ATG CTC TAC ACC ACG CCG AAC ACC TGG GTG GAC GAT 2846
 414 Y   A   G   I   H   R   S   V   M   L   Y   T   T   P   N   T   W   V   D   D   433
2847 ATC ACC GTG GTG ACG CAT GTC GCG CAA GAC TGT AAC CAC GCG TCT GTT GAC TGG CAG GTG 2906
 434 I   T   V   V   T   H   V   A   Q   D   C   N   H   A   S   V   D   W   Q   V   453
2907 GTG GCC AAT GGT GAT GTC AGC GTT GAA CTG CGT GAT GCG GAT CAA CAG GTG GTT GCA ACT 2966
 454 V   A   N   G   D   V   S   V   E   L   R   D   A   D   Q   Q   V   V   A   T   473
2967 GGA CAA GGC ACT AGC GGG ACT TTG CAA GTG GTG AAT CCG CAC CTC TGG CAA CCG GGT GAA 3026
 474 G   Q   G   T   S   G   T   L   Q   V   V   N   P   H   L   W   Q   P   G   E   493
3027 GGT TAT CTC TAT GAA CTG TGC GTC ACA GCC AAA AGC CAG ACA GAG TGT GAT ATC TAC CCG 3086
 494 G   Y   L   Y   E   L   C   V   T   A   K   S   Q   T   E   C   D   I   Y   P   513
3087 CTT CGC GTC GGC ATC CGG TCA GTG GCA GTG AAG GGC CAA CAG TTC CTG ATT AAC CAC AAA 3146
 514 L   R   V   G   I   R   S   V   A   V   K   G   Q   Q   F   L   I   N   H   K   533
3147 CCG TTC TAC TTT ACT GGC TTT GGT CGT CAT GAA GAT GCG GAC TTA CGT GGC AAA GGA TTC 3206
 534 P   F   Y   F   T   G   F   G   R   H   E   D   A   D   L   R   G   K   G   F   553
3207 GAT AAC GTG CTG ATG GTG CAC GAC CAC GCA TTA ATG GAC TGG ATT GGG GCC AAC TCC TAC 3266
 554 D   N   V   L   M   V   H   D   H   A   L   M   D   W   I   G   A   N   S   Y   573
3267 CGT ACC TCG CAT TAC CCT TAC GCT GAA GAG ATG CTC GAC TGG GCA GAT GAA CAT GGC ATC 3326
 574 R   T   S   H   Y   P   Y   A   E   E   M   L   D   W   A   D   E   H   G   I   593
3327 GTG GTG ATT GAT GAA ACT GCT GCT GTC GGC TTT TCG CTC TCT TTA GGC ATT GGT TTC GAA 3386
 594 V   V   I   D   E   T   A   A   V   G   F   S   L   S   L   G   I   G   F   E   613
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FIGURE 12 (cont'd)

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3387 GCG GGC AAC AAG CCG AAA GAA CTG TAC AGC GAA GAG GCA GTC AAC GGG GAA ACT CAG CAA 3446
 614 A   G   N   K   P   K   E   L   Y   S   E   E   A   V   N   G   E   T   Q   Q   633
3447 GCG CAC TTA CAG GCG ATT AAA GAG CTG ATA GCG CGT GAC AAA AAC CAC CCA AGC GTG GTG 3506
 634 A   H   L   Q   A   I   K   E   L   I   A   R   D   K   N   H   P   S   V   V   653
3507 ATG TGG AGT ATT GCC AAC GAA CCG GAT ACC CGT CCG CAA GGT GCA CGG GAA TAT TTC GCG 3566
 654 M   W   S   I   A   N   E   P   D   T   R   P   Q   G   A   R   E   Y   F   A   673
3567 CCA CTG GCG GAA GCA ACG CGT AAA CTC GAC CCG ACG CGT CCG ATC ACC TGC GTC AAT GTA 3626
 674 P   L   A   E   A   T   R   K   L   D   P   T   R   P   I   T   C   V   N   V   693
3627 ATG TTC TGC GAC GCT CAC ACC GAT ACC ATC AGC GAT CTC TTT GAT GTG CTG TGC CTG AAC 3686
 694 M   F   C   D   A   H   T   D   T   I   S   D   L   F   D   V   L   C   L   N   713
3687 CGT TAT TAC GGA TGG TAT GTC CAA AGC GGC GAT TTG GAA ACG GCA GAG AAG GTA CTG GAA 3746
 714 R   Y   Y   G   W   Y   V   Q   S   G   D   L   E   T   A   E   K   V   L   E   733
3747 AAA GAA CTT CTG GCC TGG CAG GAG AAA CTG CAT CAG CCG ATT ATC ATC ACC GAA TAC GGC 3806
 734 K   E   L   L   A   W   Q   E   K   L   H   Q   P   I   I   I   T   E   Y   G   753
3807 GTG GAT ACG TTA GCC GGG CTG CAC TCA ATG TAC ACC GAC ATG TGG AGT GAA GAG TAT CAG 3866
 754 V   D   T   L   A   G   L   H   S   M   Y   T   D   M   W   S   E   E   Y   Q   773
3867 TGT GCA TGG CTG GAT ATG TAT CAC CGC GTC TTT GAT CGC GTC AGC GCC GTC GTC GGT GAA 3926
 774 C   A   W   L   D   M   Y   H   R   V   F   D   R   V   S   A   V   V   G   E   793
3927 CAG GTA TGG AAT TTC GCC GAT TTT GCG ACC TCG CAA GGC ATA TTG CGC GTT GGC GGT AAC 3986
 794 Q   V   W   N   F   A   D   F   A   T   S   Q   G   I   L   R   V   G   G   N   813
3987 AAG AAA GGG ATC TTC ACT CGC GAC CGC AAA CCG AAG TCG GCG GCT TTT CTG CTG CAA AAA 4046
 814 K   K   G   I   F   T   R   D   R   K   P   K   S   A   A   F   L   L   Q   K   833
4047 CGC TGG ACT GGC ATG AAC TTC GGT GAA AAA CCG CAG CAG GGA GGC AAA CAA TGA ATCAACAA 4108
 834 R   W   T   G   M   N   F   G   E   K   P   Q   Q   G   G   K   Q   *           851
4109 CTCTCCTGGCGCACCATCGTCGGCTACAGCCTCGGTGGAATTCGATATCAAGCTTaaataagtatgaactaaaatgcatg 4188
4189 taggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataataactgagctccatctcacttc 4268
4269 ttctatgaataaacaaaggatgttatgatatattaacactctatctatgcaccttattgttctatgataaatttcctctt 4348
4349 attattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaacaaatgtgtactataagacttt 4428
4429 ctaaacaattctaactttagcattgtgaacgagacataagtgttaagaagacataacaattataatggaagaagtttgtc 4508
4509 tccatttatatattatatattacccacttatgtattatattaggatgttaaggagacataacaattataaagagagaagt 4588
4589 ttgtatccatttatatattatatactacccatttatatattatacttatccacttatttaatgtctttataaggtttgat 4668
4669 ccatgatatttctaatattttagttgatatgtatatgaaagggtactatttgaactctcttactctgtataaaggttgga 4748
4749 tcatccttaaagtgggtctatttaattttattgcttcttacagataaaaaaaaaattatgagttggtttgataaaatatt 4828
4829 gaaggatttaaaataataataaataataaataacatataatatatgtatataaatttattataatataacatttatctat 4908
4909 aaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaattatttaaacgagagtaaac 4988
4989 atatttgacttttttggttatttaacaaattattatttaacactatatgaaatttttttttttttatcggcaaggaaataaa 5068
5069 attaaattaggagggacaatggtgtgtcccaatccttatacaaccaacttccacaggaaggtcaggtcggggacaacaaa 5148
5149 aaaacaggcaagggaaatttttttaatttgggttgtcttgtttgctgcataatttatgcagtaaaacactacacataaccc 5228
5229 ttttagcagtagagcaatggttgaccgtgtgcttagcttcttttatttttatttttttatcagcaaagaataaataaaata 5308
5309 aaatgagacacttcagggatgtttcaacccttatacaaaaccccaaaaacaagtttcctagcaccctaccaactaaGGTA 5388
5389 CC                                                                              5390
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FIGURE 13

Histochemical staining of β-Glucuronidase (GUS) activity in flax embryos bombarded with vectors pBluescriptIIKS+ (negative control), pSBS2098 (GUS) pSBS2037 (oleosinGUS), and pSBS2601 (caleosinGUS).